

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3884 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (E) ORGANISM: human
- (F) CELLCYPE: chondrocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

CAGGTCAAGAACCGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTGCCCTG
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 GTCCAGTCTTGCTAGTCGTACCTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGGAC

a	M E L P F V T H L F L P L -
	GTGTTCTGACAGGTCTCTGCTCCCCCTTAACCTGGATGAACATCACCCACGCCTATT
61	61 -----+-----+-----+-----+-----+-----+-----+ 120 CACAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGGTGCGGATAAG
a	V F L T G L C S P F N L D E H H P R L F -
	CCAGGGCCACCAGAACGCTGAATTGGATACAGTGTCTTACAACATGTTGGGGTGGACAG
121	121 -----+-----+-----+-----+-----+-----+-----+ 180 GGTCCCCTGGTCTCGACTTAAACCTATGTCACAGAAATGTTGTACAACCCCCACCTGTC
a	P G P P E A E F G Y S V L Q H V G G G Q -
	CGATGGATGCTGGGGCGCCCCCTGGGATGGGCCTTCAGGGCACCGGAGGGGGACGTT
181	181 -----+-----+-----+-----+-----+-----+-----+ 240 GCTACCTACGACCACCCGGGGGACCTACCCGGAAAGTCCGCTGGCTCCCCCTGCAA
a	R W M L V G A P W D G P S G D R R G D V -
	TATCGCTGCCCTGTAGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGAC
241	241 -----+-----+-----+-----+-----+-----+-----+ 300 ATAGCGACGGGACATCCCCCCCCGGTGTACGGGTACACGGTCCGGTGAATCCACTG
a	Y R C P V G G A H N A P C A K G H L G D -
	TACCAACTGGGAAATTCTCATCTCATCCTGCTGTGAATATGCACCTGGGATGTCTCTGTTA
301	301 -----+-----+-----+-----+-----+-----+-----+ 360 ATGGTTGACCCCTTTAAGTAGAGTAGGACGACACTTACGTGGACCCCTACAGAGACAAT
a	Y Q L G N S S H P A V N M H L G M S L L -
	GAGACAGATGGTGTAGGGGGATTCTATGCCCTGTGCCCTCTCTGGTCTCGTGGTTGTGGC
361	361 -----+-----+-----+-----+-----+-----+-----+ 420 CTCTGTCTACCACTACCCCTAACGTACCGGACACGGGGAGAGACCAGAGCACGAAACACCG
a	E T D G D G G F M A C A P L W S R A C G -

AGCTCTGCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAA
 421 TCGAGACAGAAGTCAGAACCCCTATAACACGGGCACACCTACGAAGTAAGGTCGGAGTCCTCCT 480

a S S V F S S G I C A R V D A S F Q P Q G -

AGCCTGGCACCCACTGCCAACGCTGCCAACATACATGGATGTTGTCATTGCTTGGAT
 481 TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTACAACAGTAACAGAACCTA 540

a S L A P T A Q R C P T Y M D V V I V L D -

GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCATCGAAGACTGGTAGGG
 541 CCGAGGGTTGTCGTAGATGGGACCAGACTCAAGTCTGGAAGGGATGCTTCTGACCATCCC 600

a G S N S I Y P W S E V Q T F L R R L V G -

AAACTGTTATTGACCCAGAACAGATACAGGTGGACTGGTACAGTATGGGAGAGCCCT
 601 TTTGACAAAATAACTGGGTCTTGCTATGTCACCCCTGACCATGTCATAACCCCTCTCGGGGA 660

a K L F I D P E Q I Q V G L V Q Y G E S P -

GTACATGAGTGGTCCCTGGGAGATTCCGAACGAAGGAAGAAGTGGTAGAGAGCAGCAAAG
 661 CATGTAACCACTCACCAGGGACCCCTAAAGGCTTGCCTCCTTCTCACCACCTCTCGTCGTTTC 720

a V H E W S L G D F R T K E E V V R A A K -

AACCTCAGTCGGCGGGAGGGACGAGAAACAAAGACTGCCAAGCAATAATGGTGGCCTGC
 721 TTGGAGTCAGCCGCCCTCCCTGCTCTTGTCTGACGGGTTCGTTATTACCAACCGGACG 780

a N L S R R E G R E T K T A Q A I M V A C -

ACAGAAGGGTTCAGTCAGTCCCATGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT
 781 TGTCTCCCAAGTCAGTCAGGTACCCCCGGCTGGCTCCGACGGTCCGATGACCACCAA 840

a T E G F S Q S H G G R P E A A R L L V V -

GTCACTGATGGAGAGTCCCAGTGGAGAGGGAGCTTCCTGCAGCACTAAAGGCTGTGAG
 841 CAGTGACTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCGTGATTTCGGGACACTC 900

a V T D G E S H D G E E L P A A L K A C E -

GCTGGAAGAGTGACACGCTATGGGATTGCAGTCCTGGTCACTACCTCCGGCGGCAGCGA
 901 CGACCTTCTCACTGTGCGATAACCTAACGTCAAGGAACCAAGTGATGGAGGCCGCGCT 960

a A G R V T R Y G I A V L G H Y L R R Q R -

GATCCCAGCTTTCTGAGAGAAATTAGAACTATTGCCAGTGATCAGATGAGCGATTG
 961 CTAGGGTCGAGAAAGGACTCTTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG 1020

a D P S S F L R E I R T I A S D P D E R F -

TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG
 1021 AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCCTCTAGCC 1080

a F F N V T D E A A L T D I V D A L G D R -

1081 ATTTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTGGGCTGGAAATGTCT
 TAAAAACCGAACCTCCCAGGGTACGTCTTGCTTCGAGGAAACCCGACCTTACAGA 1140

a I F G L E G S H A E N E S S F G L E M S -

1141 CAGATTGGTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTGGGATGGTGGGGGCC
 GTCTAACCAAAGAGGTGAGTAGCCGATTCCTACCCCTAACGAAAAACCTACCACCCCCGG 1200

a Q I G F S T H R L K D G I L F G M V G A -

1201 TATGACTGGGGAGGCTCTGTGCTATGGCTTAAGGAGGCCACCGCCTTTCCCCCACGA
 ATACTGACCCCTCCGAGACACGATAACGAACCTCCTCCGGTGGCGGAAAGGGGGTGCT 1260

a Y D W G G S V L W L E G G H R L F P P R -

1261 ATGGCACTGGAAGACGAGTTCCCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTTAC
 TACCGTGACCTTCTGCTCAAGGGGGGACGTGACGTCTGGTACGTGGATGGACCCAATG 1320

a M A L E D E F P P A L Q N H A A A Y L G Y -

1321 TCTGTTCTTCCATGCTTTCGGGGTGGACGCCGCCTGTTCTCTCTGGGCTCCTCGA
 AGACAAAGAAGGTACGAAACGCCACCTGCGCGGACAAAGAGAGACCCCGAGGAGCT 1380

a S V S S M L L R G G R R L F L S G A P R -

1381 TTTAGACATCGAGGAAAAGTCATGCCCTCCAGCTTAAGAAAGATGGGCTGTGAGGGTT
 AAATCTGTAGCTCCTTTCAGTAGCGGAAGGTGAATTCTTCTACCCGACACTCCCAA 1440

a F R H R G K V I A F Q L K K D G A V R V -

1441 GCCCAGAGCCTCCAGGGGGAGCAGATTGGTCATACTTGGCAGTGAGCTCTGCCATTG
 CGGGTCTCGGAGGTCGGCTAACCAAGTATGAAACCGTCACTCGAGACGGTAAC 1500

a A Q S L Q G E Q I G S Y F G S E L C P L -

1501 GATACAGATAGGGATGGAACAACACTGATGTCCTACTTGTGGCTGCCCATGTTCTGGGA
 CTATGTCTATCCCTACCTGTTGACTACAGAACACCGACGGGGTACAAGGACCCCT 1560

a D T D R D G T T D V L L V A A P M F L G -

1561 CCCCAGAACAGGAAACAGGACGTGTTATGTATCTGGTAGGCCAGTCCTGCTG
 GGGGTCTGTTCTTGTGCTGACAAATACACATAGACCATCGGGTCAGGAACGAC 1620

a P Q N K E T G R V Y V Y L V G Q Q S L L -

1621 ACCCTCCAAGAACACTTCAGCCAGAACCCCCCAGGATGCTCGGTTGGCTTGCCATG
 TGGGAGGTTCTGTGAAGTCGGCTTGGGGGGCTACGAGCCAAACCGAACGGTAC 1680

a T L Q G T L Q P E P P Q D A R F C F A M -

1681 GGAGCTCTCCTGATCTGAACCAAGATGGTTTGCTGATGTGGCTGTGGGGCGCCTCTG
 CCTCGAGAAGGACTAGACTTGGTCTACAAAACGACTACACCGAACACCCCCGGAGAC 1740

a G A L P D L N Q D G F A D V A V G A P L -

1741 GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCC
 CTTCTACCGTGGTCCCTCGTGACATGGACATGGTACCTGGTCTCACCTCAGTCCGGG +-----+ 1800
 a E D G H Q G A L Y L Y H G T Q S G V R P -
 CATCCTGCCAGAGGATTGCTGCTGCCATGCCACATGCCCTCAGCTACTTGGCCGA
 1801 GTAGGAOGGGTCTCCAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGCT +-----+ 1860
 a H P A Q R I A A A S M P H A L S Y F G R -
 AGTGTGGATGGTCGGCTAGATCTGGATGGAGATGATCTGGTCGATGTGGCTGTGGGTGCC
 1861 TCACACCTACCAGCCGATCTAGACCTACCTACTAGACCAGCTACACCGACACCCACGG +-----+ 1920
 a S V D G R L D L D G D D L V D V A V G A -
 CAGGGGGCAGCCATCCTGCTCAGCTCCCGCCATTGTCCATCTGACCCCACACTGGAG
 1921 GTCCCCCGTCGGTAGGACGAGTCGAGGGCCGGTAACAGGTAGACTGGGTAGTGACCTC +-----+ 1980
 a Q G A A I L L S S R P I V H L T P S L E -
 GTGACCCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGC GGCGAGGCCAAGAACCA
 1981 CACTGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCCGCTCGGTTCTCGT +-----+ 2040
 a V T P Q A I S V V Q R D C R R R G Q E A -
 GTCTGTCTGACTGCAGCCCTTGCTTCCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT
 2041 CAGACAGACTGACGTCGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCTA +-----+ 2100
 a V C L T A A L C F Q V T S R T P G R W D -
 CACCAATTCTACATGAGGTTACCGCATCACTGGATGAATGGACTGCTGGGCACGTGCA
 2101 GTGGTTAAGATGTACTCCAAGTGGCTAGTGACCTACTTACCTGACGACCCCGTGCACGT +-----+ 2160
 a H Q F Y M R F T A S L D E W T A G A R A -
 GCATTTGATGGCTCTGGCCAGAGGTTGTCGGAGGCTCCGGCTCAGTGTGGGAAT
 2161 CGTAAACTACCGAGACCGGTCTCAAACAGGGAGCCTCCGAGGCCGAGTCACACCCCTTA +-----+ 2220
 a A F D G S G Q R L S P R R L R L S V G N -
 GTCACTTGTGAGCAGCTACACTTCCATGTGCTGGATACTCAGATTACCTCCGGCCAGTG
 2221 CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGGCGGTAC +-----+ 2280
 a V T C E Q L H F H V L D T S D Y L R P V -
 GCCTTGACTGTGACCTTGCCTGGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG
 2281 CGGAACTGACACTGGAAACGGAACCTGTTATGATGTTCGGTCCCGACACGACTTACTC +-----+ 2340
 a A L T V T F A L D N T T K P G P V L N E -
 GGCTCACCCACCTCTATACAAAGCTGGTCCCTTCTCAAAGGATTGTGGCCCTGACAAT
 2341 CCGAGTGGGTGGAGATATGTTTCGACCAGGGAAAGAGTTCTAACACCGGGACTGTTA +-----+ 2400
 a G S P T S I Q K L V P F S K D C G P D N -

40

a GAATGTGTCACAGACCTGGTGCTCAAGTGAATATGGACATCAGAGGCTCCAGGAAGGCC 2401 2460
 CTTACACAGTGTCTGGACCACGAAGTTCACTTATACTGTAGTCCTCGAGGTCCCTCCGG

a E C V T D L V L Q V N M D I R G S R K A -
 CCATTGAGGTGGCCGGAAAGTGCTGGTATCTACAACCTCTGGAGAACAGA 2461 2520
 GGTAAACACCAAGCTCCACCGGCCCTTCACGACCATAGATGTTGAGACCTCTGTCT

a P F V V R G G R R K V L V S T T L E N R -
 AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTCTCTAGAAACCTCCACCTGGCC 2521 2580
 TTCCTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTGGAGGTGGACCGG

a K E N A Y N T S L S I I F S R N L H L A -
 AGTCTCACTCCTCAGAGAGAGAGCCCATAAAGGTGGAATGTGCCGCCCTCTGCTCAT 2581 2640
 TCAGAGTGAGGAGCTCTCTCTCGGGTTATTCACACGGCGGGGAAGACGAGTA

a S L T P Q R E S P I K V E C A A P S A H -
 GCCCGGCTCTGCAGTGTGGGGCATCCTGTTCCAGACTGGAGCCAAGGTGACCTTCTG 2641 2700
 CGGGCCGAGACGTACACCCCGTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

a A R L C S V G H P V F Q T G A K V T F L -
 CTAGAGTTGAGTTAGCTGCTCCTCTCTCTGAGCCAGGTCTTGGGAAGCTGACTGCC 2701 2760
 GATCTCAAACCTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCTTCGACTGACGG

a L E F E F S C S S L L S Q V F G K L T A -
 AGCAGTGACAGCCTGGAGAGAAATGGCACCCCTCAAGAAAACACAGCCCAGACCTCAGCC 2761 2820
 TCGTCACTGTCGGACCTCTCTTACCGTGGGAAGTCCTTTGTGTCGGTCTGGAGTCGG

a S S D S L E R N G T L Q E N T A Q T S A -
 TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCCCTGCACCGCTATGAG 2821 2880
 ATGTAGGTTATACTCGGGTGGAGGACAAGAGATCACTCAGATGGACGTGGCGATACTC

a Y I Q Y E P H L L F S S E S T L H R Y E -
 GTTCACCCATATGGGACCCCTCCAGTGGTCCTGGCCAGAATTCAAAACACTCTCAGG 2881 2940
 CAAGTGGGTATAACCTGGGAGGGTCACCCAGGACCGGGCTTAAAGTTGGTGGAGAGTC

a V H P Y G T L P V G P G P E F K T T L R -
 GTTCAGAACCTAGGCTGCTATGTGGTCAGTGGCCTCATCATCTCACCCCTCCTCCAGCT 2941 3000
 CAAGTCTGGATCCGACGATAACCCAGTCACCGAGTAGTAGAGTCGGAGGAAGGTCGA

a V Q N L G C Y V V S G L I I S A L L P A -
 GTGGCCCATGGGGCAATTACTCCTATCACTGTCTCAAGTCATCACTAACATGCAAGC 3001 3060
 CACCGGGTACCCCGTTAATGAAGGATAGTGACAGAGTTCACTGAGTCAGTAGTGTACGTTCG

a V A H G G N Y F L S L S Q V I T N N A S -

41

3061 TGCATAGTGCAGAACCTGACTGAACCCCCAGGCCACCTGTGCATCCAGAGGAGCTCAA
 ACGTATCACGTCTGGACTGACTTGGGGTCCGGGTGACACGTAGGTCTCTCGAAGTT 3120

a C I V Q N L T E P P G P P V H P E E L Q -

3121 CACACAAACAGACTGAATGGGAGCAATACTCAGTGTCAAGTGGTGAGGTGCCACCTGGG
 GTGTGTTGTCTGACTTACCTCGTTATGAGTCACAGTCCACCACCTCACGGTGGAACCC 3180

a H T N R L N G S N T Q C Q V V R C H L G -

3181 CAGCTGGCAAAGGGGACTGAGGTCTCTGTTGGACTATTGAGGTGGTCACAATGAATT
 GTCGACCGTTTCCCTGACTCCAGAGACAACCTGATAACTCCGACCAAGTGTACTTAAA 3240

a Q L A K G T E V S V G L L R L V H N E F -

3241 TTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTGAGCTGGAACCGAA
 AAGGCTTCTCGGTTCAAGTTCAAGGGACTGCCACCAGTCGTGGAAACTCGACCCCTGGCTT 3300

a F R R A K F K S L T V V S T F E L G T E -

3301 GAGGGCAGTGTCTACAGCTGACTGAAGCCTCCGTTGGAGTGAGAGCCTTGGAGGTG
 CTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTCTCGGAGAACCTCCAC 3360

a E G S V L Q L T E A S R W S E S L L E V -

3361 GTTCAGACCCGGCTATCCTCATCTCCCTGATCCTCATAGGCAGTGTCTGGAGGG
 CAAGTCTGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCGTACAGGACCCCTCCC 3420

a V Q T R P I L I S L W I L I G S V L G G -

3421 TTGCTCCTGCTTGCTCTCCTTGTCTTCTGACTGTGGAAAGCTTGGCTTCTTGCCCATAAG
 AACGAGGACGAACGAGAGGAACAGAACAGACCGAACCTCGAACCGAAGAACGGTATTTC 3480

a L L L L A L L V F C L W K L G F F A H K -

3481 AAAATCCCTGAGGAAGAAAAAGAGAAGAGAAGTTGGAGCAATGAATGTAGAATAAGGGT
 TTTTAGGGACTCCTCTTTCTCTCTCAACCTCGTTACTACATCTTATTCCCA 3540

a K I P E E E K R E E K L E Q

3541 CTAGAAAGTCCTCCCTGGCAGCTTCTTCAAGAGACTTGCATAAAAGCAGAGGTTGGGG
 GATCTTCAGGAGGGACCGTCGAAAGAAGTTCTCTGAACGTATTTCGTCTCCAAACCCC 3600

3601 GCTCAGATGGGACAAGAACGCCCTCTGGACTATCTCCAGACAGCAGCCTGACTTGA
 CGAGTCTACCCCTGTTCTCGGGAGACCTGATAGAGGGTCTGGTCTCGGACTGAACCT 3660

3661 CTTTGAGTCCTAGGGATGCTGGTAGAGATGAGGCTTACCTCAGACAAGAACAGC
 GAAAACTCAGGATCCCTACGACGACCGATCTACTCCGAAATGGAGTCTGTTCTCG 3720

42

3721 TGGCACCAAAACTAGCCATGCTCCCACCCCTTGCTTCCCTCCTCGTGATCCTGGTTC
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3780
ACCGTGGTTTGATCGGTACGAGGGTGGGAGACGAAGGGAGGAGGAGCACTAGGACCAAG

3781 CATAGCCAACACTGGGGCTTTGTTGGGTCCCTTATCCCCAGGAATCAATAATT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3840
GTATCGGTTGTGACCCCGAACAAACCCAGGAAATAGGGGTCCCTAGTTATTAAAAA

3841 TTGCCTAGGAAAAAAAAAGCGGCCGCAATTGATATCAAGCT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3884
AACGGATCCTTTTTTCGCGCGCTTAAGCTATAGTCGA

(2) INFORMATION FOR SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3779 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (E)

(i) MOLECULAR TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human

- (B) CELLYTYPE: chondrocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

	CAGGTCAAGAACCGATCAGGCATGGAACTCCCTTCGTCACTCACCTGTTCTGCCCTG	60
1	-----+-----+-----+-----+-----+-----+	
	GTCCAGTCTTGCTAGTCGTACCTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGAC	
	M E L P F V T H L F L P L -	
	GTGTT CCTGACAGGTCTCTGCTCCCCCTTAACCTGGATGAACATCACCCACGCCATT	120
61	-----+-----+-----+-----+-----+-----+	
	CACAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGTGC GGATAAG	
a	V F L T G L C S P F N L D E H H P R L F -	
	CCAGGGCCACCAGAACGCTGAATTGGATACAGTGTCTAACACATGTTGGGGTGGACAG	180
121	-----+-----+-----+-----+-----+-----+	
	GGTCCC CGGTGGTCTCGACTAACCTATGTACAGAACATGTTGTACAACCCCCACCTGTC	
a	P G P P E A E F G Y S V L Q H V G G G Q -	
	CGATGGATGCTGGTGGCGCCCCCTGGATGGGCCTTCAGCGACCGGAGGGGGACGTT	240
181	-----+-----+-----+-----+-----+-----+	
	GCTACCTACGACCACCCCGCGGGGGAC CCTACCCGGAA GTCCGCTGGCCTCCCCCTGCAA	
a	R W M L V G A P W D G P S G D R R G D V -	
	TATCGCTGCCCTGTAGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGAC	300
241	-----+-----+-----+-----+-----+-----+	
	ATAGCGACGGGACATCCCCCCC GG GTTACGGGTACAGGTTCCCGGTGAATCCACTG	
a	Y R C P V G G A H N A P C A K G H L G D -	
	TACCAACTGGGAAATTCTCATCCTCATGGCTGTGAATATGCACCTGGGATGTCCTGTTA	360
301	-----+-----+-----+-----+-----+-----+	
	ATGGTTGACCC TTAAAGTAGAGTAGGACGACACTTATACGTGGACCCCTACAGAGACAAT	
a	Y Q L G N S S H P A V N M H L G M S L L -	
	GAGACAGATGGTGTGGGGATT CATGGCCTGTGCCCTCTCTGGTCTCGTGCTTGTGGC	420
361	-----+-----+-----+-----+-----+-----+	
	CTCTGTCTACCACTACCCCTAAGTACCGGACACGGGGAGAGACCAGAGCACGAACACCG	
a	E T D G D G G F M A C A P L W S R A C G -	
	AGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGG	480
421	-----+-----+-----+-----+-----+-----+	
	TCGAGACAGAAGTCAAGACCCCTATACACGGGCACACCTACGAAGTAAGGTGGAGTCCCT	

44

a S S V F S S G I C A R V D A S F Q P Q G -
 481 AGCCTGGCACCCACTGCCAACGCTGCCAACATACTGGATGTTGTCAATTGTCATTGGAT
 TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTAACAGTAACAGAACCTA 540

a S L A P T A Q R C P T Y M D V V I V L D -
 541 GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAAGACCTCCTACGAAGAGACTGGTAGGG
 CCGAGGTTGTCGTAGATGGGGACCAGACTCAAGTCTGGAAGGATGCTTCTGACCATCCC 600

a G S N S I Y P W S E V Q T F L R R L V G -
 601 AAACTGTTATTGACCCAGAACAGATAACAGGTGGACTGGTACAGTATGGGGAGAGCCCT
 TTTGACAAATAACTGGGTCTTGCTATGTCCACCCCTGACCATGTCATACCCCTCTCGGGA 660

a K L F I D P E Q I Q V G L V Q Y G E S P -
 661 GTACATGAGTGGTCCCTGGGAGATTCCGAAACGAAGGAAGTGGTGAGAGCAGCAAAG
 CATGTACTCACCAGGGACCCCTCTAAAGGCTTGCTTCCCTTCACCACTCTCGTCGTTTC 720

a V H E W S L G D F R T K E E V V R A A K -
 721 AACCTCAGTCGGCGGGAGGGACCGAGAACAAAGACTGCCAACATAATGGTGGCCTGC
 TTGGAGTCAGCCGCCCTCCCTGCTTTGTTCTGACGGGTTCGTTATTACCAACCGGACG 780

a N L S R R E G R E T K T A Q A I M V A C -
 781 ACAGAAGGGTTCAAGTCAGTCCCATGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT
 TGTCTCCAAGTCAGTCAGGGTACCCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA 840

a T E G F S Q S H G G R P E A A R L L V V -
 841 GTCACTGATGGAGAGTCCCCTGATGGAGAGGGAGCTTCTGCAGCACTAAAGGCTGTGAG
 CAGTGACTACCTCTCAGGGTACTACCTCTCGAAGGACGTCGTGATTTCCGGACACTC 900

a V T D G E S H D G E E L P A A L K A C E -
 901 GCTGGAAGAGTGCACCGCTATGGGATTGCACTGGTCACTACCCCTCCGGCGGCAGCGA
 CGACCTCTCACTGTGCGATACCCCTAACGTCAGGAACCAAGTGTGATGGAGGCCGCGTCGCT 960

a A G R V T R Y G I A V L G H Y L R R Q R -
 961 GATCCCAGCTTTCTGAGAGAAAATTAGAACTATTGCCAGTGATCCAGATGAGCGATT
 CTAGGGTCGAGAAAGGACTCTCTTAATCTGATAACGGTCACTAGGTCTACTCGCTAAAG 1020

a D P S S F L R E I R T I A S D P D E R F -
 1021 TTCTTCAATGTCAAGATGAGGCTGCTCTGACTGACATTGGGATGCACTAGGAGATCGG
 AAGAAGTTACAGTGTCACTCCGACGAGACTGACTGTAACACCTACGTGATCTCTAGCC 1080

a F F N V T D E A A L T D I V D A L G D R -
 1081 ATTTTGCCCTTGAGGGTCCCATGCAGAAAAGCAAAGCTCCTTGGGCTGGAAATGTCT
 TAAAAACCGGAACCTCCAGGGTACGTCTTGCTTGCAGGAAACCCGACCTTACAGA 1140

45

a I F G L E G S H A E N E S S F G L E M S -
 1141 CAGATTGGTTCTCCACTCATCGGCTAAAGGATGGATTCTTTGGATGGTGGGGGCC
 GTCTAACCAAGAGGTGAGTAGCCGATTTCTACCCCTAACGAAAACCCTACCACCCCCGG 1200

a Q I G F S T H R L K D G I L F G M V G A -
 1201 TATGACTGGGGAGGCCTCTGCTATGGCTGAAGGAGGCCACCGCTTTCCCCCACGA
 ATACTGACCCCTCCGAGACACGATACCGAACTTCCTCCGGTGGCGAAAAGGGGGGTGCT 1260

a Y D W G G S V L W L E G G H R L F P P R -
 1261 ATGGCACTGGAACACGAGTTCCCCCTGCAGCAGAACCATGCAGCCTACCTGGTTAC
 TACCGTGACCTTCTGCTCAAGGGGGACGTGACGTCTGGTACGTCGGATGGACCCAATG 1320

a M A L E D E F P P A L Q N H A A Y L G Y -
 1321 TCTGTTCTTCCATGCCTTGCGGGGTGGACGCCGCCTGTTCTCTGGGCTCCTCGA
 AGACAAAGAAGGTACGAAACGCCACCTGCGCGAACAAAGAGAGACCCGAGGAGCT 1380

a S V S S M L L R G G R R L F L S G A P R -
 1381 TTTAGACATCGAGGAAAAGTATCGCCTCCAGCTTAAGAAAGATGGGCTGTGAGGGTT
 AAATCTGTAGCTCCTTTCACTGCGGAAGGTGCAATTCTTCTACCCGACACTCCCAA 1440

a F R H R G K V I A F Q L K K D G A V R V -
 1441 GCCCAGAGCCTCCAGGGGGAGCAGATTGGTCATACTTGGCAGTGAGCTGCCCATTG
 CGGGTCTCGGAGGTCCCCCTCGCTAACCAAGTATGAAACCGTCACTCGAGACGGGTAAC 1500

a A Q S L Q G E Q I G S Y F G S E L C P L -
 1501 GATACAGATAGGGATGGAACAACGTGATGTTACTTGTGGCTGCCCATGTTCTGGG
 CTATGTCTATCCCTACCTGTTGACTACAGAATGAACACCGACGGGGTACAAGGACCC 1560

a D T D R D G T T D V L L V A A P M F L G -
 1561 CCCCAGAACAGGAAACAGGACGTGTTATGTATCTGGTAGGCCAGCAGTCCTGCTG
 GGGGTCTTGTCTTGTGACACATAGACCATCCGGTCGTAGGAACCGAC 1620

a P Q N K E T G R V Y V Y L V G Q Q S L L -
 1621 ACCCTCCAAGGAACACTTCAGCCAGAACCCCCCAGGATGCTCGGTTGGCTTGCATG
 TGGGAGGTTCTGTGAAGTCGGTCTGGGGGGTCTACGAGCAAACCGAACGGTAC 1680

a T L Q G T L Q P E P P Q D A R F G F A M -
 1681 GGAGCTCTCCTGATCTGAACCAAGATGGTTGCTGATGTTGGCTGTGGGGCGCCTCTG
 CCTCGAGAAGGACTAGACTTGGTCTACCAAAACGACTACACCGACACCCCGCGGAGAC 1740

a G A L P D L N Q D G F A D V A V G A P L -
 1741 GAAGATGGGCACCAAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCC
 CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTGGTCTCACCTCAGTCCGGG 1800

46

a E D G H Q G A L Y L Y H G T Q S G V R P -
 1801 CATCCTGCCACAGGATTGCTGCTGCCATGCCACATGCCCTCAGCTACTTGGCGA
 GTAGGACGGGTCTCTAACGACGACGGAGGTACGGTGTACGGAGTCGATGAAACCGGCT 1860

a H P A Q R I A A A S M P H A L S Y F G R -
 1861 AGTGTGGATGGTCGGTAGATCTGGATGGAGATGATCTGGTCGATGTGGCTGTGGTGCC
 TCACACCTACCAGCCGATCTAGACCTACCTACTAGACCAAGCTACACCGACACCCACGG 1920

a S V D G R L D L D G D D L V D V A V G A -
 1921 CAGGGGGCAGCCATCCTGCTCAGCTCCGGCCATTGTCCATCTGACCCCCTCACTGGAG
 GTCCCCCGTCGGTAGGACGACTCGAGGGCCGGTAACAGGTAGACTGGGTAGTGACCTC 1980

a Q G A A I L L S S R P I V H L T P S L E -
 1981 GTGACCCCACAGGCCATCAGTGTGGTTCAAGAGGGACTGTAGGCAGGCAAGAAGCA
 CACTGGGTGTCGGTAGTCACACCAAGTCTCCCTGACATCCGCCCTCCGGTTCTCGT 2040

a V T P Q A I S V V Q R D C R R R G Q E A -
 2041 GTCTGTCGACTGCAGCCCTTGCTTCAAGTGAACCTCCGTACTCCTGGTCGCTGGAT
 CAGACAGACTGACGTCGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCCCTA 2100

a V C L T A A L C F Q V T S R T P G R W D -
 2101 CACCAATTCTACATGAGGTTCACCGCATCACTGGATGAATGGACTGCTGGGCACGTGCA
 GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTACCTGACGACCCCGTGCACGT 2160

a H Q F Y M R F T A S L D E W T A G A R A -
 2161 GCATTTGATGGCTCTGCCAGAGGTTGTCGGCTCAGGAGGCTCCGGCTCAGTGTGGGAAT
 CGTAAACTACCGAGACCGGTCTCCAACAGGGAGGCTCCGAGGCCAGTCACACCCCTTA 2220

a A F D G S G Q R L S P R R L R L S V G N -
 2221 GTCACTTGTGAGCAGCTACACTCCATGTGGATAACATCAGATTACCTCCGGCCAGTG
 CAGTGAACACTCGTCGATGTGAAGGTACAGGACCTATGAGTCTAATGGAGGCCGGTCAC 2280

a V T C E Q L H F H V L D T S D Y L R P V -
 2281 GCCTTGACTGTGACCTTGGCTTGGACAATACTACAAAGCCAGGGCTGTGCTGAATGAG
 CGGAACACTGGAAACGGAACCTGTTATGATGTTGGTCCGGACACGACTTACTC 2340

a A L T V T F A L D N T T K P G P V L N E -
 2341 GGCTCACCCACCTCTACAAAAGCTGGTCCCTCTCAAAGGATTGTGGCCCTGACAAT
 CCGAGTGCGGTGGAGATATGTTTCGACCAGGGGAAGAGTTCCCTAACACCGGGACTGTTA 2400

a G S P T S I Q K L V P F S K D C G P D N -
 2401 GAATGTGTACAGACCTGGTCTCAAGTGAATATGGACATCAGAGGCTCCAGGAAGGCC
 CTTACACAGTGTCTGGACCACGAAGTTCACTTACCTGAGTCTCCGAGGTCCCTCCGG 2460

47

a E C V T D L V L Q V N M D I R G S R K A -
 2461 CCATTTGTGGTTTCGAGGTGGCCGGCGGAAAGTGCTGGTATCTACAACTCTGGAGAACAGA 2520
 GGTAAACACCAAGCTCCACCGGCCCTTCACGACCATAAGATGTTGAGACCTCTGTCT

a P F V V R G G R R K V L V S T T L E N R -
 2521 AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTCTCTAGAAACCTCACCTGGCC 2580
 TTCCCTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTGGAGGTGGACCGG

a K E N A Y N T S L S I I F S R N L H L A -
 2581 AGTCTCACTCCTCAGAGAGAGAGCCAATAAAGGTGAATGTGCCGCCCTCTGCTCAT 2640
 TCAGAGTGGAGGAGTCTCTCTCGGGTATTCCACCTACACGGCGGGAAAGACGAGTA

a S L T P Q R E S P I K V E C A A P S A H -
 2641 GCCCGGCTCTGCAGTGTGGGGCATCCTGCTTCCAGACTGGAGCCAAGGTGACCTTCTG 2700
 CGGGCCGAGACGTACACCCCGTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

a A R L C S V G H P V F Q T G A K V T F L -
 2701 CTAGAGTTGAGTTAGCTGCTCCTCTCCCTGAGCCAGGTCTTGGGAAGCTGACTGCC 2760
 GATCTCAAACCTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCCCTCGACTGACGG

a L E F E F S C S S L L S Q V F G K L T A -
 2761 AGCAGTGACAGCCTGGAGAGAAATGGCACCCCTCAAGAAAACACAGCCCAGACCTCAGCC 2820
 TCGTCACTGTCGGACCTCTTTACCGTGGGAAGTTCTTTGTGTCGGGTCTGGAGTCGG

a S S D S L E R N G T L Q E N T A Q T S A -
 2821 TACATCCAATATGAGCCCCACCTCCTGTTCTAGTGAGTCTACCCCTGCACCGCTATGAG 2880
 ATGTAGGTTATACTCGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGATACTC

a Y I Q Y E P H L L F S S E S T L H R Y E -
 2881 GTTCACCCATATGGGACCCCTCCAGTGGGTCTGGCCCAAGAATTCAAACCACTCTCAGG 2940
 CAAGTGGGTATAACCTGGGAGGGTCACCCAGGACCGGGCTTAAGTTTGGTGAGAGTCC

a V H P Y G T L P V G P G P E F K T T L R -
 2941 ACTAACAAATGCAAGCTGCATAGTGCAGAACCTGACTGAACCCCOAGGCCACCTGTGCAT 3000
 TGATTGTTACGTTCGACGTATCACGTCTGGACTGACTTGGGGTCCGGGTGGACACGTA

a T N N A S C I V Q N L T E P P G P P V H -
 3001 CCAGAGGAGCTTCAACACACAAACAGACTGAATGGGAGCAATACTCACTGTCAAGTGGTG 3060
 GGTCTCCTCGAAGTTGTGTTGTCTGACTTACCCCTCGTTATGAGTCACAGTCCACAC

a P E E L Q H T N R L N G S N T Q C Q V V -
 3061 AGGTGCCACCTGGCAGCTGGCAAAGGGACTGAGGTCTCTGTTGGACTATTGAGGCTG 3120
 TCCACGGTGGAACCCGTCGACCGTTCCCTGACTCCAGAGACAAACCTGATAACTCCGAC

48

a R C H L G Q L A K G T E V S V G L L R L -
 3121 GTTCACAATGAATT TTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTT
 CAAAGTGTACTTAAAAAGGCTCTCGGTTCAAGTCAGGGACTGCCACCAGTCGTGGAAA 3180

a V H N E F F R R A K F K S L T V V S T F -
 3181 GAGCTGGGAACCGAAGAGGGCAGTGTCCCTACAGCTGACTGAAGCCTCCCCTGGAGTGAG
 CTCGACCCCTGGCTCTCCCGTACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTC 3240

a E L G T E E G S V L Q L T E A S R W S E -
 3241 AGCCTCTGGAGGTGGTCAGACCCGGCTATCCTCATCTCCCTGTGGATCCTCATAGGC
 TCGGAGAACCTCCACCAAGTCTGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCG 3300

a S L L E V V Q T R P I L I S L W I L I G -
 3301 AGTGTCTGGGAGGGTTGCTCCTGCTTGCTCTCCTGTCTCTGCCTGTGGAGCTTGGC
 TCACAGGACCCCTCCAAACGAGGACGARCGAGAGGAACAGAACGGACACCTTCGAACCG 3360

a S V L G G L L L A L L V F C L W K L G -
 3361 TTCTTTGCCATAAGAAAATCCCTGAGGAAGAAAAAGAGAACAGAGAGTTGGAGCAATGA
 AAGAAACGGGTATTCTTTAGGGACTCCTCTTTCTCTCTCAACCTCGTTACT 3420

a F F A H K K I P E E E K R E E K L E Q
 3421 ATGTAGAATAAGGGCTAGAAAGTCCTCCCTGGCAGCTTCTTAAGAGACTTGCATAAA
 TACATCTTATTCCCAGATCTTCAGGAGGGACCGTCGAAAGAAGTCTCTGAACGTATTT 3480

3481 AGCAGAGGTTGGGGCTCAGATGGACAAGAAGCCGCTCTGGACTATCTCCCCAGACC
 TCGTCTCAAACCCCGAGTCTACCCCTGTTCTCGCCGGAGACCTGATAGAGGGTCTGG 3540

3541 AGCAGCTGACTTGACTTTGAGTCCTAGGGATGCTGGCTAGAGATGAGGCTTACCC
 TCGTCGGACTGAACTGAAACTCAGGATCCCTACGACGACCGATCTACTCCGAAATGG 3600

3601 TCAGACAAGAAGAGCTGGCACCAAAACTAGCCATGCTCCACCCCTGCTTCCCTCC
 AGTCTGTTCTCTCGACCGTGGTTTGATCGGTACGAGGGTGGAGACGAAGGGAGGAGG 3660

3661 TCGTGATCCTGGTCCATAGCCAACACTGGGGCTTTGTTGGGTCTTTATCCCCAG
 AGCACTAGGACCAAGGTATCGGTTGTGACCCGAAAACAAACCCAGGAAAATAGGGGTC 3720

3721 GAATCAATAATTTTTGCCTAGGAAAAAAAAAGCGGCCGCAATTGATATCAAGCT
 CTTAGTTATTAAAAACGGATCCTTTTTCGCCGGCGCTTARGCTATAAGTCGA 3779

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(2) INFORMATION FOR SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULAR TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) CELLTYPE: chondrocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

NdeI
|
GGGGCATATGGTTCAGAACCTGGGTTGCTACGTTGTTCCGGTCTGATCATCTCGCTCT
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
CCCCGTATAACCAAGTCTGGACCCAACGATGCAACAAAGGCCAGACTAGTAGAGGCGAGA

b G H M V Q N L G C Y V V S G L I I S A L -
|
GCTGCCCGCTGTTGCTCACGGTGGTAACTAACCTCCTAACGCTTGTCAGGTTATCAGCGG
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
CGACGGCCGACAACCGAGTGCCACCATTGATGAAGGATTGAAACAGGGTCCAATAGTCGCC

b L P A V A H G G N Y F L S L S Q V I S G -
|
BamHI
|
CCTGGTGCCGCGCGATCCCCCCC
121 -----+-----+-----+-----+-----+-----+-----+ 143
GGACCAACGGCGCGCTAGGGGGG

b L V P R G S P -